CLAIMS

1. Method for high throughput analysis of data sets generally described by sets of peaks characterized by a position and an area.

2. Method according to claim 1 characterized in that bioinformatic tools are used to extract and smooth peak data sets according to parameter files and store them in data files.

3. Method according to claim 1 and 2 characterized in that particular profiles representing peaks will be created to be analyzed.

4. Method according to claims 1 to 3 characterized in that peak database is built.

5. Method according to claims 1 to 4 characterized in that peak database is analyzed by statistical tools.

6. Method according to claims 1 to 5 characterized in that analysis of peak database will be used to determine prognostic or diagnostic criteria.

7. Method according to claims 1 to 6 in that the prognostic and diagnostic criteria are used in the field of physiopathology such as immunotheraphy, cancer treatment, HIV, infectious disease, autoimmune disease.

8. Method according to claims 1 to 7 characterized in that the method is a high throughput method for analysis of immune repertoires.

9. Method according to claim 8 characterized by:

starting with biological samples, which contains DNA or RNA fragments

purifying DNA or RNA fragments.

10. The method according to claim 9, further comprising

synthesizing cDNA from purified RNA

on purified DNA or cDNA performing amplification of DNA by PCR or SDA

methods by using oligonucleotides specific for antigen specific receptor genes e.g.

Immunoglobulin and T-cell receptor, variable (V), Junctional (J) and Constant (c) regions

on amplified DNA performing a labeling step for detection e.g. by performing a

runoff extension step with J or C specific oligonucleotide labeled with a fluorescent drug

on each labeled amplified DNA, an electrophoretic separation is made on an

automatic sequencer

5   for each eletrophoregram, identifying peaks by determining their position and area

that correspond to labeled amplified DNA.

11. Method according to claim 9 charaterized in that the method of analysis is based

on the reading of the labeled amplified DNA is the method according to claims 1 to 8.

10   12. A computer program product, comprising:

a computer storage medium; and

a computer program code mechanism embedded in the computer storage medium for

causing a computer to produce an analysis of raw data produced by a separation technique for

biomolecules, the computer program code mechanism having

15   a first computer code device configured to extract a first set of raw data and a

second set of raw data from at least one database,

a second computer code device configured to determine a first value from the

first set of raw data corresponding to a first characteristic and a second value from the second

set of raw data corresponding to the first characteristic, and

20   a third computer code device configured to store the first value and the second

value in a memory.

13. The computer program product of Claim 12, wherein the computer program code

mechanism further has

a fourth computer code device configured to retrieve the first value and the

second value from the memory and to order the first value and the second value based on a

user preference stored in a second memory.

5   14. The computer program product of Claim 13, wherein the computer program code

mechanism further has

          a fifth computer code device configured to produce a graphical representation

of the first value and the second value as ordered by the fourth computer code device.

10   15. The computer program product of Claim 13, wherein the computer program code

mechanism further has

          a fourth computer code device configured to smooth at least one of the first set of raw

data and the second set of raw data produced by the separation technique for biomolecules.

15   16. The computer program product of Claim 13, wherein the computer program code

mechanism further has

          a fifth computer code device configured to format at least one of the first value and

the second value.

20   17. The computer program product of Claim 12, wherein the computer program code

mechanism further has

          a fourth computer code device configured to parameterize at least one of the first set

of raw data and the second set of raw data.

18. The computer program product of Claim 12, wherein the computer program code mechanism further has

a fourth computer code device, configured to analyze at least one of the first set of raw data and the second set of raw data.

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19. The computer program product of Claim 12, wherein the computer program code mechanism further has

a fourth computer code device, configured to export at least one of the first value and the second value.

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20. The computer program product of Claim 12, wherein the first characteristic comprises a peak.

21. The computer program product of Claim 12, wherein the separation technique for

15   biomolecules comprises polynucleotide sequencing.

22. The computer program product of Claim 21, wherein the polynucleotide is DNA.

23. A device, comprising:

20   at least one extractor configured to extract raw data produced by a separation technique for biomolecules, the extractor including

a processor, and

a computer readable medium encoded with processor readable instructions that, when executed by the processor implement,

an extraction mechanism configured to extract a first set of raw data

and a second set of raw data from at least one database,

a characteristic determining mechanism configured to determine a first

value from the first set of raw data corresponding to a first characteristic and a second value

5   from the second set of raw data corresponding to the first characteristic, and

an output mechanism configured to store the first value and the second

value in a memory.

24. A system, comprising:

10   a digital repository populated with entries of raw data produced by a separation

technique for biomolecules;

a processor; and

a computer readable medium encoded with processor readable instructions that, when

executed by the processor implement,

15   an extraction mechanism configured to extract a first set of raw data and a

second set of raw data from the digital repository,

a characteristic determining mechanism configured to determine a first value

from the first set of raw data corresponding to a first characteristic and a second value from

the second set of raw data corresponding to the first characteristic, and

20   an output mechanism configured to store the first value and the second value

in a memory.

25. A system, comprising:

a digital repository populated with entries of raw data produced by a separation

25   technique for biomolecules;

a processor; and

a computer readable medium encoded with processor readable instructions that, when

executed by the processor implement,

an extraction mechanism configured to extract a first set of raw data and a

5   second set of raw data from the digital repository via a network,

a characteristic determining mechanism configured to determine a first value

from the first set of raw data corresponding to a first characteristic and a second value from

the second set of raw data corresponding to the first characteristic, and

an output mechanism configured to store the first value and the second value

10   in a memory.

26. The system of Claim 25, wherein at least a portion of the network comprises an

Internet protocol network.

15   27. The system of Claim 26, wherein at least a portion of the network comprises the

Internet.

28. A computer data signal embodied in a carrier wave, said computer data signal

comprising extracted raw data produced by a separation technique for biomolecules.

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29. A computer data signal embodied in a carrier wave, said computer data signal

comprising:

smoothed raw data, wherein the raw data includes data produced by a separation

technique for biomolecules.

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30. A computer data signal embodied in a carrier wave, said computer data signal comprising:

formatted raw data, wherein the raw data includes data produced by a separation technique for biomolecules.

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31. A computer data signal embodied in a carrier wave, said computer data signal comprising:

parameterized raw data, wherein the raw data includes data produced by a separation technique for biomolecules..

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32. A computer data signal embodied in a carrier wave, said computer data signal comprising:

analyzed raw data, wherein the raw data includes data produced by a separation technique for biomolecules.

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33. A computer data signal embodied in a carrier wave, said computer data signal comprising:

exported raw data, wherein the raw data includes data produced by a separation technique for biomolecules.

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34. A software package, wherein said software package is embodied by the ISEApeaks package 2.0.1.

35. A method comprising:

25   a) isolating a biological sample;

b) extracting raw data from the biological sample; and

c) compiling the raw data into a database using ISEApeaks.

36. The method of Claim 35, wherein said biological sample is selected from the group consisting of a growth culture, an electrophoretic sample, a chromatographic column, a blotting membrane, a centrifugation tube, or a microarray chip.

37. The method of Claim 35, wherein said biological sample comprises one or more biomolecule.

38. The method of Claim 37, wherein said biomolecule is selected from the group consisting of intact cells, cellular material, DNA, RNA and proteins.

39. The method of Claim 37, wherein said biomolecule is labeled.

40. The method of Claim 35, wherein said isolating is a technique selected from the group consisting of centrifugation, precipitation, batch adsorption, chromatography, electrophoresis, and a microarray chip.

41. The method of Claim 35, wherein said extracting comprises using a bioinformatics tool.

42. The method of Claim 41, wherein said bioinformatics tool is selected from the group consisting of GENESCAN™, MMUNOSCOPE™, GENOTESTER™, IMAGEQUANT™, EAGLESIGHT™, QUANTITYONE™, and MICROARRAY SUITE™.

43. The method of Claim 35, further comprising analyzing said raw data using ISEApeaks.

5   44. A device for diagnostic or prognostic applications comprising

         (a) a set of oligonucleotides for describing TC Receptor or Immunoglobulin repertoires;

         (b) a reference database of TC Receptor or Immunoglobulin repertoires data; and

         (c) written or informatic guidelines for obtaining results from the sample to be
10   analyzed.

         45. The method according to Claim 35, wherein the biological sample is isolated from a mammal.